

SEQUENCE LISTING

<110> Sagami Chemical Research Center,

Protegene Inc.

5

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661925

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<150> JP 11-188835

<151> 1999-07-02

<160> 30

15

<210> 1

<211> 233

<212> PRT

<213> Homo sapiens

20

<400> 1

Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu Leu Leu Gly Ser

1

5

10

15

Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn

25

20

25

30

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Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu
 35 40 45
 Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile
 50 55 60
 5 Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val
 65 70 75 80
 Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn
 85 90 95
 Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp
 10 100 105 110
 Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
 115 120 125
 Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
 130 135 140
 15 Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
 145 150 155 160
 Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
 165 170 175
 Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
 20 180 185 190
 Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
 195 200 205
 Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
 210 215 220
 25 Cys Asp Phe Pro Ser Phe Asn Leu Lys

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225 230

<210> 2

<211> 273

5 <212> PRT

<213> Homo sapiens

<400> 2

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
10 1 5 10 15
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
20 25 30
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
35 40 45
15 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
50 55 60
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
65 70 75 80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
20 85 90 95
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
100 105 110
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
115 120 125
25 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg

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130 135 140
 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
 145 150 155 160
 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
 5 165 170 175
 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
 180 185 190
 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
 195 200 205
 10 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
 210 215 220
 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
 225 230 235 240
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
 15 245 250 255
 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
 260 265 270
 Ser

20 <210> 3
 <211> 282
 <212> PRT
 <213> Homo sapiens.

25 <400> 3

5 /59

	Met	Ser	Gly	Ser	Ser	Leu	Pro	Ser	Ala	Leu	Ala	Leu	Ser	Leu	Leu	Leu
	1				5					10					15	
	Val	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Pro	Gly	Ala	Ala	Gln	Asn	Glu	Pro
					20					25					30	
5	Arg	Ile	Val	Thr	Ser	Glu	Glu	Val	Ile	Ile	Arg	Asp	Ser	Pro	Val	Leu
					35					40					45	
	Pro	Val	Thr	Leu	Gln	Cys	Asn	Leu	Thr	Ser	Ser	Ser	His	Thr	Leu	Thr
					50					55					60	
	Tyr	Ser	Tyr	Trp	Thr	Lys	Asn	Gly	Val	Glu	Leu	Ser	Ala	Thr	Arg	Lys
10		65				70					75				80	
	Asn	Ala	Ser	Asn	Met	Glu	Tyr	Arg	Ile	Asn	Lys	Pro	Arg	Ala	Glu	Asp
						85					90				95	
	Ser	Gly	Glu	Tyr	His	Cys	Val	Tyr	His	Phe	Val	Ser	Ala	Pro	Lys	Ala
					100					105					110	
15	Asn	Ala	Thr	Ile	Glu	Val	Lys	Ala	Ala	Pro	Asp	Ile	Thr	Gly	His	Lys
					115					120					125	
	Arg	Ser	Glu	Asn	Lys	Asn	Glu	Gly	Gln	Asp	Ala	Thr	Met	Tyr	Cys	Lys
					130					135					140	
	Ser	Val	Gly	Tyr	Pro	His	Pro	Asp	Trp	Ile	Trp	Arg	Lys	Lys	Glu	Asn
20		145				150					155				160	
	Gly	Met	Pro	Met	Asp	Ile	Val	Asn	Thr	Ser	Gly	Arg	Phe	Phe	Ile	Ile
						165					170				175	
	Asn	Lys	Glu	Asn	Tyr	Thr	Glu	Leu	Asn	Ile	Val	Asn	Leu	Gln	Ile	Thr
					180						185				190	
25	Glu	Asp	Pro	Gly	Glu	Tyr	Glu	Cys	Asn	Ala	Thr	Asn	Ala	Ile	Gly	Ser

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195 200 205
 Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala Pro Leu
 210 215 220
 Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val Val Ile
 5 225 230 235 240
 Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro Asp Asp
 245 250 255
 Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn His Lys
 260 265 270
 10 Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn
 275 280

<210> 4

<211> 238

15 <212> PRT

<213> Homo sapiens

<400> 4

Met Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu
 20 1 5 10 15
 Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
 20 25 30
 Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
 35 40 45
 25 Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr

7

	50	55	60
	Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys		
	65	70	75 80
	Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser		
5	85	90	95
	Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala		
	100	105	110
	Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val		
	115	120	125
10	Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly		
	130	135	140
	Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn		
	145	150	155 160
	Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser		
15	165	170	175
	Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val		
	180	185	190
	His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln		
	195	200	205
20	Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp		
	210	215	220
	His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala		
	225	230	235
25	<210> 5		

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<211> 372

<212> PRT

<213> Homo sapiens

5 <400> 5

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro

1 5 10 15

Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val

20 25 30

10 Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu

35 40 45

Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu

50 55 60

Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser

15 65 70 75 80

Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr

85 90 95

Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu

100 105 110

20 Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg

115 120 125

Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly

130 135 140

Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His

25 145 150 155 160

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	Arg	Pro	Ser	Arg	Cys	Arg	Tyr	Arg	Asp	Leu	Glu	Val	Arg	Leu	Cys	Phe
					165					170					175	
	Glu	Ser	Phe	Ser	Asp	Glu	Leu	Trp	Lys	Gly	Arg	Leu	Leu	Pro	Leu	Val
				180					185					190		
5	Leu	Leu	Ala	Glu	Ala	Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Val	Val
				195				200					205			
	Tyr	Ser	Ser	Gly	Arg	Val	Phe	Trp	Thr	Leu	Ala	Arg	Pro	Asp	Ala	Thr
				210				215					220			
	Gln	Ser	Gln	Arg	Arg	Arg	Lys	Thr	Val	Arg	Leu	Leu	Leu	Ala	Asn	Leu
10		225				230					235				240	
	Val	Ile	Phe	Leu	Leu	Cys	Phe	Val	Pro	Tyr	Asn	Ser	Thr	Leu	Ala	Val
				245						250				255		
	Tyr	Gly	Leu	Leu	Arg	Ser	Lys	Leu	Val	Ala	Ala	Ser	Val	Pro	Ala	Arg
				260						265				270		
15	Asp	Arg	Val	Arg	Gly	Val	Leu	Met	Val	Met	Val	Leu	Leu	Ala	Gly	Ala
				275					280					285		
	Asn	Cys	Val	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ala	Glu	Gly	Phe
				290				295					300			
	Arg	Asn	Thr	Leu	Arg	Gly	Leu	Gly	Thr	Pro	His	Arg	Ala	Arg	Thr	Ser
20		305				310					315				320	
	Ala	Thr	Asn	Gly	Thr	Arg	Ala	Ala	Leu	Ala	Gln	Ser	Glu	Arg	Ser	Ala
				325						330				335		
	Val	Thr	Thr	Asp	Ala	Thr	Arg	Pro	Asp	Ala	Ala	Ser	Gln	Gly	Leu	Leu
				340						345				350		
25	Arg	Pro	Ser	Asp	Ser	His	Ser	Leu	Ser	Ser	Phe	Thr	Gln	Cys	Pro	Gln

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355

360

365

Asp Ser Ala Leu

370

5 <210> 6

<211> 146

<212> PRT

<213> Homo sapiens

10 <400> 6

Met Trp Lys Leu Trp Arg Ala Glu Glu Gly Ala Ala Ala Leu Gly Gly

1

5

10

15

Ala Leu Phe Leu Leu Leu Phe Ala Leu Gly Val Arg Gln Leu Leu Lys

20

25

30

15 Gln Arg Arg Pro Met Gly Phe Pro Pro Gly Pro Pro Gly Leu Pro Phe

35

40

45

Ile Gly Asn Ile Tyr Ser Leu Ala Ala Ser Ser Glu Leu Pro His Val

50

55

60

Tyr Met Arg Lys Gln Ser Gln Val Tyr Gly Glu Val Gln Pro Arg Arg

20

65

70

75

80

Ala Pro Gly Arg Glu Gly Arg Gln Ala Gly Pro Gly Trp Pro Gly Pro

85

90

95

Ser Trp Leu Asp Leu Trp Pro Pro Leu Gly Arg Leu Val Gly Thr Ser

100

105

110

25 Pro Cys Ala Gly Cys Pro Leu Arg Asp Thr Arg Phe Pro Gly Leu Glu

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115 120 125
Gly Arg Ser Pro Arg Arg Arg Ala Pro Leu Gln Gly Glu Pro Arg Pro
130 135 140
Cys Arg
5 145

<210> 7
<211> 302
<212> PRT
10 <213> Homo sapiens

<400> 7
Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
1 5 10 15
15 Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu
20 25 30
Cys Leu Ala Thr Cys Leu Asp His His Phe Pro Thr Gly Ser Arg Pro
35 40 45
Thr Val Pro Gly Pro Leu His Phe Ser Gly Tyr Ser Ser Val Pro Asp
20 50 55 60
Gly Lys Pro Leu Val Arg Glu Pro Cys Arg Ser Cys Ala Val Val Ser
65 70 75 80
Ser Ser Gly Gln Met Leu Gly Ser Gly Leu Gly Ala Glu Ile Asp Ser
85 90 95
25 Ala Glu Cys Val Phe Arg Met Asn Gln Ala Pro Thr Val Gly Phe Glu

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	100	105	110
	Ala Asp Val Gly Gln Arg Ser Thr Leu Arg Val Val Ser His Thr Ser		
	115	120	125
	Val Pro Leu Leu Leu Arg Asn Tyr Ser His Tyr Phe Gln Lys Ala Arg		
5	130	135	140
	Asp Thr Leu Tyr Met Val Trp Gly Gln Gly Arg His Met Asp Arg Val		
	145	150	155
	Leu Gly Gly Arg Thr Tyr Arg Thr Leu Leu Gln Leu Thr Arg Met Tyr		
	165	170	175
10	Pro Gly Leu Gln Val Tyr Thr Phe Thr Glu Arg Met Met Ala Tyr Cys		
	180	185	190
	Asp Gln Ile Phe Gln Asp Glu Thr Gly Lys Asn Arg Arg Gln Ser Gly		
	195	200	205
	Ser Phe Leu Ser Thr Gly Trp Phe Thr Met Ile Leu Ala Leu Glu Leu		
15	210	215	220
	Cys Glu Glu Ile Val Val Tyr Gly Met Val Ser Asp Ser Tyr Cys Arg		
	225	230	235
	Glu Lys Ser His Pro Ser Val Pro Tyr His Tyr Phe Glu Lys Gly Arg		
	245	250	255
20	Leu Asp Glu Cys Gln Met Tyr Leu Ala His Glu Gln Ala Pro Arg Ser		
	260	265	270
	Ala His Arg Phe Ile Thr Glu Lys Ala Val Phe Ser Arg Trp Ala Lys		
	275	280	285
	Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp Arg Thr Glu		
25	290	295	300

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<210> 8

<211> 194

<212> PRT

5 <213> Homo sapiens

<400> 8

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
1 5 10 15
10 Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
20 25 30
Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
35 40 45
Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
15 50 55 60
Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
65 70 75 80
Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
85 90 95
20 Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
100 105 110
Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
115 120 125
Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
25 130 135 140

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Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala

145

150

155

160

Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys

165

170

175

5 Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His

180

185

190

Gly Phe

10 <210> 9

<211> 542

<212> PRT

<213> Homo sapiens

15 <400> 9

Met Lys Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe

1

5

10

15

Leu Ser Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser

20

25

30

20 Tyr Ser Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn

35

40

45

Trp Ala Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser

50

55

60

Val Asn Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn

25

65

70

75

80

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	Ile Val Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His	
	85	90 95
	Asn Thr Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr	
	100	105 110
5	Thr Glu Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg	
	115	120 125
	Lys Leu Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr	
	130	135 140
	Leu Gly Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro	
10	145	150 155 160
	Arg Gln Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu	
	165	170 175
	Gln Glu Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala	
	180	185 190
15	Arg Ala Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu	
	195	200 205
	Lys Ala Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg	
	210	215 220
	Cys Asn Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser	
20	225	230 235 240
	Lys Ser Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu	
	245	250 255
	Ser Val Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr	
	260	265 270
25	Val Trp Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val	

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	275	280	285
	Cys Ile Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe		
	290	295	300
	Ile Ile Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys		
5	305	310	315
	Val Ala Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe		
	325	330	335
	Trp Met Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile		
	340	345	350
10	Phe Arg Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile		
	355	360	365
	Gly Tyr Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr		
	370	375	380
	Glu Pro Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp		
15	385	390	395
	Asp Asn Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile		
	405	410	415
	Val Ala Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln		
	420	425	430
20	Arg Pro Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met		
	435	440	445
	Arg Ile Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr		
	450	455	460
	Trp Gly Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe		
25	465	470	475
			480

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His Ile Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu

485

490

495

Leu Phe Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met

500

505

510

5 Arg Met Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser

515

520

525

Leu Gly Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly

530

535

540

10 <210> 10

<211> 276

<212> PRT

<213> Homo sapiens

15 <400> 10

Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu

1

5

10

15

Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro

20

25

30

20 Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala

35

40

45

Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala

50

55

60

Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser

25

65

70

75

80

	Arg Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro		
	85	90	95
	Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp		
	100	105	110
5	Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val		
	115	120	125
	Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn		
	130	135	140
	Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met		
10	145	150	155
	Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile		
	165	170	175
	Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly		
	180	185	190
15	Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu		
	195	200	205
	Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe		
	210	215	220
	Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly		
20	225	230	235
	Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu		
	245	250	255
	Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro		
	260	265	270
25	Ser Leu Ser Pro		

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275

<210> 11

<211> 699

5 <212> DNA

<213> Homo. sapiens

<400> 11

	atgtggcagc ttttagcagc agcatgctgg atgcttcttc ttggatctat gtatggttat	60
10	gacaagaaag gaaacaatgc aaacctgaa gctaatatga atattagcca gattatttct	120
	tactgggggtt atccttatga agagtatgat gttacaacaa aagatggtta tacccttgga	180
	atttatagga ttccacatgg aagaggatgc ccaggaggga cagctccaaa gcctgctgtg	240
	tatttgcagc atggcttaat tgcatctgcc agtaactgga ttgcaacct gcccaacaac	300
	agtttggctt tccttctggc agatagtggg tatgacgtgt ggttggggaa cagccgagga	360
15	aacacttggg ccagaaaaca ccttaaattg tcaccgaaat caccagaata ctgggccttc	420
	agtttggatg agatggctaa atatgacctt ccagccacaa tcaattttat catagagaaa	480
	actggacaga agcgactcta ctacgtgggc cactcacaag gcaccacat agcttttata	540
	gcattttcta caaaccaga actggctaaa aagattaaga tattttttgc actggctcca	600
	gttgtcacag ttaaatacac ccaaagtcct atgaaaaaac taacaaccct ttccaggcga	660
20	gtagttaagg tatgtgactt cccaagtttt aatctgaaa	699

<210> 12

<211> 819

<212> DNA

25 <213> Homo sapiens

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<400> 12

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	gagcacgcct accggcccgg ccgtaggggtg tgtgctgtcc gggctcacgg ggaccctgtc	120
5	tccgagtcgt tcgtgcagcg tgtgtaccag cccttcctca ccacctgca cgggcaccgg	180
	gcctgcagca cctaccgaac catctatagg accgcctacc gccgcagccc tgggctggcc	240
	cctgccaggc ctcgctacgc gtgctgcccc ggctggaaga ggaccagcgg gcttcctggg	300
	gcctgtggag cagcaatatg ccagccgcca tgccggaacg gagggagctg tgtccagcct	360
	ggccgctgcc gctgccctgc aggatggcgg ggtgacactt gccagtcaga tgtggatgaa	420
10	tgcagtgcta ggaggggagg ctgtccccag cgctgcgtca acaccgccgg cagttactgg	480
	tgccagtgtt gggaggggca cagcctgtct gcagacggta cactctgtgt gccaaggga	540
	gggcccccca ggggtggccc caaccgaca ggagtggaca gtgcaatgaa ggaagaagtg	600
	cagaggctgc agtccagggt ggacctgtg gaggagaagc tgcagctggt gctggcccca	660
	ctgcacagcc tggcctcgca ggcaactggag catgggctcc cggaccccg cagcctcctg	720
15	gtgcactcct tccagcagct cggccgcacg gactccctga gcgagcagat ttccttcctg	780
	gaggagcagc tggggtcctg ctctgcaag aaagactcg	819

<210> 13

<211> 846

20 <212> DNA

<213> Homo sapiens

<400> 13

	atgtcgggtt cgctcgtgcc cagcgccctg gccctctcgc tgttgctggt ctctggctcc	60
25	ctcctcccag ggccaggcgc cgctcagaac gagccaagga ttgtcaccag tgaagaggtc	120

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	attattcgag acagccctgt tctccctgtc accctgcagt gtaacctcac ctccagctct	180
	cacaccctta catacagcta ctggacaaag aatgggggtgg aactgagtgc cactcgtaag	240
	aatgccagca acatggagta caggatcaat aagccgagag ctgaggattc aggcgaatac	300
	cactgcgtat atcactttgt cagcgtcctt aaagcaaacg ccaccattga agtgaaagcc	360
5	gctcctgaca tcaactggcca taaacggagt gagaacaaga atgaagggca ggatgccact	420
	atgtattgca agtcagttgg ctacccccac ccagactgga tatggcgcaa gaaggagaac	480
	gggatgcccc tggacattgt caatacctct ggccgcttct tcatcatcaa caaggaaaat	540
	tacactgagt tgaacattgt gaacctgcag atcacggaag accctggcga gtatgaatgt	600
	aatgccacca acgccattgg ctccgcctct gttgtcactg tcctcagggt gcggagccac	660
10	ctggccccac tctggccttt cttgggaatt ctggctgaaa ttatcatcct tgttggtgatc	720
	attgttgtgt atgagaagag gaagaggcca gatgaggttc ctgacgatga tgaaccagct	780
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	acaaat	846
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	<213> Homo sapiens	
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	atggtggagg tgcagctgga cgctgaccac gactaccac ccgggctgct catcgcttc	180
	agtgcctgca ccacagtgtt ggtggctgtg cacctgtttg cgctcatgat cagcacctgc	240
25	atcctgcccc acatcgaggc ggtgagcaac gtgcacaatc tcaactcggc caaggagtcc	300

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 5 gtgcccttcg gcctgatctt tategtcttc gccgtccact tctaccgctc actggttagc 600
 cataagaccg accgacagtt ccaggagctc aacgagctgg cggagtttgc ccgcttacag 660
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10 <211> 1116

<212> DNA

<213> Homo sapiens

<400> 15

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 gacgagctgt ggaaaggcag gctgctgccc ctctgctgc tggccgaggc gctgggcttc 600
 25 ctgctgcccc tggcgggcgt ggtctactcg tcgggccgag tcttctggac gctggcgcg 660

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 gtcattcttc tgctgtgctt cgtgccctac aacagcacgc tggcggctta cgggctgctg 780
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 gccaccaacg ggacgcgggc ggcgctcgcg caatccgaaa ggtccgccgt caccaccgac 1020
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 <211> 438
 <212> DNA
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 cttccccatg tctacatgag aaagcagagc caggtgtacg gagaggtaca gccccgacgg 240
 20 gccccgggca gggagggccg ccaggctggc ccgggctggc cagggccttc ctggttgac 300
 ttatggccgc ccctgggccc actagtcggg acctctccgt gtgccggctg ccctttgagg 360
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25 <210> 17

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<211> 906

<212> DNA

<213> Homo sapiens

5 <400> 17

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cacttcccca caggctccag gccactgtg ccgggacccc tgcacttcag tggatatagc 180
agtgtgccag atgggaagcc gctgggtccgc gagccctgcc gcagctgtgc cgtggtgtcc 240
10 agctccggcc aaatgctggg ctccaggcctg ggtgtgtgaga tcgacagtgc cgagtgcgtg 300
ttccgcatga accaggcgcc caccgtgggc tttgaggcgg atgtgggcca gcgcagcacc 360
ctgcgtgtcg tctcacacac aagcgtgccg ctgtgtgtgc gcaactattc acactacttc 420
cagaaggccc gagacacgct ctacatggtg tggggccagg gcaggcacat ggaccgggtg 480
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cagatgtacc tggcacacga gcaggcgccc cgaagcgccc accgcttcac cactgagaag 840
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actgag 906

<210> 18

<211> 582

25 <212> DNA

25 /59

<213> Homo sapiens

<400> 18

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ggaagacgct acggcctgaa ctactgtgga gttcgtgctt ctgaaaggct ggctgaaata 180
gacatgccat acctcctgaa atatcaaccc atgatgcaaa ccattggcca aaagtactgc 240
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10 tggattagtg agtctcaggt ttcccagaca actgaagttc tgactactag aatcaaagaa 420
atccagagga gggttccaac ctggaccctt gaccagtacc tgagaggtgg actctgtgcc 480
tacagtgggg gtgctggcta tgtccgaagc agccaggacc tgagctgtga cttctgcaat 540
gatgtccttg cagagccaa gtacctcaag agacatggct tc 582

15 <210> 19

<211> 1626

<212> DNA

<213> Homo sapiens

20 <400> 19

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tgttcccact atagatccaa gattcaccta aaaagctata gtgaagtggc caaccacatc 120
ctcgacacag cagccatttc aaactgggct ttcattccca acaaaaatgc cagctcggtat 180
ttgttgcaat cagtgaattt gtttgccaga caactccaca tccacaataa ttctgagaac 240
25 attgtgaatg aactcttcat tcagacaaaa gggtttcaca tcaaccataa tacctcagag 300

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 cagattccca ggcaagagct aaggaagctg tggccaaatg catccaagc cattagcata 420
 gctttcccaa ccttgggggc tctctgaga gaagcccact tgcaaaatgt gagtcttccc 480
 agacaggtaa atggctctggt gctatcagtg gttttaccag aaaggttgca agaaatcata 540
 5 ctcaccttcg aaaagatcaa taaaaccgcg aatgccagag ccagtggtgt tggctggcac 600
 tccaagaaaa ggagatggga tgagaaagcg tgccaaatga tgttgatat caggaacgaa 660
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 ctaagcttgg ttctttgcct gatcattgaa gccacagtggt ggtcccggt ggttgtagc 840
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 gacaatacca aagccctttt agcatttgcc atcccgcggt tcgtcattgt ggctgtaaat 1260
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 ctgggactga cctgggggtt tggaatagcc actctcatag aaggcacttc cttgacgttc 1440
 20 catataattt ttgccttget caatgctttc cagggttttt tcatcctget gtttgaacc 1500
 attatggatc acaagataag agatgctttg aggatgagga tgtcttcact gaaggggaaa 1560
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<211> 828

<212> DNA

<213> Homo sapiens

5 <400> 20

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gacctggaag ggaaggtcac agccaccacc ttctccctgg agcagccgcg ctgtgtcttc 180
gatgggcttg ccagcggccag cgataccgtc tggctcgtgg tggccttcag caatgcctcc 240
10 aggggcttcc agaaccggga gacactggct gacattccgg cctccccaca gctgctgacc 300
gatggccact acatgacgt gcccctgtct ccggaccagc tggcctgtgg cgaccccatg 360
gcgggcagcg gaggcgcccc cgtgctgcgg gtgggcatg accacggctg ccaccagcag 420
cccttctgca acgcgcccct ccttggccct ggaccctatc gggatgaagtt cctcctgatg 480
gacaccaggg gctcaccag ggctgagacc aagtggcag accccatcac tctccaccaa 540
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accatgcgt tctccagcct gtggtggccg gaggaggccc cggagcagct gcggatcggc 720
tccttcatgg gcaagcgcta catgaccac cacatccac ccagcgaggc cgccacactg 780
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20

<210> 21

<211> 1308

<212> DNA

<213> Homo sapiens

25

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<220>

<221> CDS

<222> (76)... (777)

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Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu

1

5

10

10 ctt ctt gga tct atg tat ggt tat gac aag aaa gga aac aat gca aac 159

Leu Leu Gly Ser Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn

15

20

25

cct gaa gct aat atg aat att agc cag att att tct tac tgg ggt tat 207

Pro Glu Ala Asn Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr

15

30

35

40

cct tat gaa gag tat gat gtt aca aca aaa gat ggt tat atc ctt gga 255

Pro Tyr Glu Glu Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly

45

50

55

60

att tat agg att cca cat gga aga gga tgc cca ggg agg aca gct cca 303

20 Ile Tyr Arg Ile Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro

65

70

75

aag cct gct gtg tat ttg cag cat ggc tta att gca tct gcc agt aac 351

Lys Pro Ala Val Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn

80

85

90

25 tgg att tgc aac ctg ccc aac aac agt ttg gct ttc ctt ctg gca gat 399

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	Trp Ile Cys Asn Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp	
	95 100 105	
	agt ggt tat gac gtg tgg ttg ggg aac agc cga gga aac act tgg tcc	447
	Ser Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser	
5	110 115 120	
	aga aaa cac ctt aaa ttg tca ccg aaa tca cca gaa tac tgg gcc ttc	495
	Arg Lys His Leu Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe	
	125 130 135 140	
	agt ttg gat gag atg gct aaa tat gac ctt cca gcc aca atc aat ttt	543
10	Ser Leu Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe	
	145 150 155	
	atc ata gag aaa act gga cag aag cga ctc tac tac gtg ggc cac tca	591
	Ile Ile Glu Lys Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser	
	160 165 170	
15	caa ggc acc acc ata gct ttt ata gca ttt tct aca aac cca gaa ctg	639
	Gln Gly Thr Thr Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu	
	175 180 185	
	gct aaa aag att aag ata ttt ttt gca ctg gct cca gtt gtc aca gtt	687
	Ala Lys Lys Ile Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val	
20	190 195 200	
	aaa tac acc caa agt cct atg aaa aaa cta aca acc ctt tcc agg cga	735
	Lys Tyr Thr Gln Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg	
	205 210 215 220	
	gta gtt aag gta tgt gac ttc cca agt ttt aat ctg aaa taacta	780
25	Val Val Lys Val Cys Asp Phe Pro Ser Phe Asn Leu Lys	

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225

230

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 agcagagttc aggggaactcc ccctgttgct aatctgccct actttcttca tctatgtcta 960
 5 gaaacgtgtc tgctgcgcca ttcctcaacc acagatagag agaacttatt tgattgattg 1020
 gtttgttgaa tttagtagat tgaatttttc tagtgatccc taatttttta ggggcagtgg 1080
 tggttgagtt cacagcatgg aatcagatgg tgtgtgtttg aatgttattt ctatgatttg 1140
 caagctgggt aaatttggtc aagaccttaa gttctcttca tctgtaatgt ggggataata 1200
 atagttctta ctcatagggc taccctgagg actaagtaaa ttaatacagc atacctcta 1260
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<210> 22

<211> 1272

<212> DNA

15 <213> Homo sapiens

<220>

<221> CDS

<222> (60)... (881)

20

<400> 22

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atg agg ggc tct cag gag gtg ctg ctg atg tgg ctt ctg gtg ttg gca 107

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala

25

1

5

10

15

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	gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg tgt gct	155
	Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala	
	20 25 30	
	gtc cgg gct cac ggg gac cct gtc tcc gag tcg ttc gtg cag cgt gtg	203
5	Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val	
	35 40 45	
	tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc agc acc	251
	Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr	
	50 55 60	
10	tac cga acc atc tat agg acc gcc tac cgc cgc agc cct ggg ctg gcc	299
	Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala	
	65 70 75 80	
	cct gcc agg cct cgc tac gcg tgc tgc ccc ggc tgg aag agg acc agc	347
	Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser	
15	85 90 95	
	ggg ctt cct ggg gcc tgt gga gca gca ata tgc cag ccg cca tgc cgg	395
	Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg	
	100 105 110	
	aac gga ggg agc tgt gtc cag cct ggc cgc tgc cgc tgc cct gca gga	443
20	Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly	
	115 120 125	
	tgg cgg ggt gac act tgc cag tca gat gtg gat gaa tgc agt gct agg	491
	Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg	
	130 135 140	
25	agg ggc ggc tgt ccc cag cgc tgc gtc aac acc gcc ggc agt tac tgg	539

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Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
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 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
 5 165 170 175
 gtg ccc aag gga ggg ccc ccc agg gtg gcc ccc aac ccg aca gga gtg 635
 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
 180 185 190
 gac agt gca atg aag gaa gaa gtg cag agg ctg cag tcc agg gtg gac 683
 10 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
 195 200 205
 ctg ctg gag gag aag ctg cag ctg gtg ctg gcc cca ctg cac agc ctg 731
 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
 210 215 220
 15 gcc tcg cag gca ctg gag cat ggg ctc ccg gac ccc ggc agc ctc ctg 779
 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
 225 230 235 240
 gtg cac tcc ttc cag cag ctc ggc cgc atc gac tcc ctg agc gag cag 827
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
 20 245 250 255
 att tcc ttc ctg gag gag cag ctg ggg tcc tgc tcc tgc aag aaa gac 875
 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
 260 265 270
 tcg tgactgccca gcgccccagg ctggactgag ccctcacgc cgccctgcag cc 930
 25 Ser

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cccatgcccc tgcccaacat gctgggggtc cagaagccac ctggggtga ctgagcggaa 990
 ggccaggcag ggcccttcctc ctcttcctcc tcccttcct cgggaggctc ccagaccct 1050
 ggcatgggat gggctgggat cttctctgtg aatccacccc tggctacccc caccctggct 1110
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 ctggagcctg ggacccatgg cacaggccag gcagcccgga ggctgggtgg ggcctcagt 1230
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<210> 23

10 <211> 2083

<212> DNA

<213> Homo sapiens

<220>

15 <221> CDS

<222> (188)... (1036)

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 tccctccct tcccggccc cggtcttgcc cccggcccat tcgtgttggt gtcttctgct 180
 agggagg atg tcg ggt tcg tcg ctg ccc agc gcc ctg gcc ctc tcg ctg 229

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu

1

5

10

25 ttg ctg gtc tct ggc tcc ctc ctc cca ggg cca ggc gcc gct cag aac 277

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	Leu	Leu	Val	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Pro	Gly	Ala	Ala	Gln	Asn	
	15					20					25					30	
	gag cca agg att gtc acc agt gaa gag gtc att att cga gac agc cct																325
	Glu	Pro	Arg	Ile	Val	Thr	Ser	Glu	Glu	Val	Ile	Ile	Arg	Asp	Ser	Pro	
5					35					40					45		
	gtt ctc cct gtc acc ctg cag tgt aac ctc acc tcc agc tct cac acc																373
	Val	Leu	Pro	Val	Thr	Leu	Gln	Cys	Asn	Leu	Thr	Ser	Ser	Ser	His	Thr	
					50					55					60		
	ctt aca tac agc tac tgg aca aag aat ggg gtg gaa ctg agt gcc act																421
10	Leu	Thr	Tyr	Ser	Tyr	Trp	Thr	Lys	Asn	Gly	Val	Glu	Leu	Ser	Ala	Thr	
			65					70						75			
	cgt aag aat gcc agc aac atg gag tac agg atc aat aag ccg aga gct																469
	Arg	Lys	Asn	Ala	Ser	Asn	Met	Glu	Tyr	Arg	Ile	Asn	Lys	Pro	Arg	Ala	
			80				85						90				
15	gag gat tca ggc gaa tac cac tgc gta tat cac ttt gtc agc gct cct																517
	Glu	Asp	Ser	Gly	Glu	Tyr	His	Cys	Val	Tyr	His	Phe	Val	Ser	Ala	Pro	
			95				100					105			110		
	aaa gca aac gcc acc att gaa gtg aaa gcc gct cct gac atc act ggc																565
	Lys	Ala	Asn	Ala	Thr	Ile	Glu	Val	Lys	Ala	Ala	Pro	Asp	Ile	Thr	Gly	
20					115					120				125			
	cat aaa cgg agt gag aac aag aat gaa ggg cag gat gcc act atg tat																613
	His	Lys	Arg	Ser	Glu	Asn	Lys	Asn	Glu	Gly	Gln	Asp	Ala	Thr	Met	Tyr	
					130					135				140			
	tgc aag tca gtt ggc tac ccc cac cca gac tgg ata tgg cgc aag aag																661
25	Cys	Lys	Ser	Val	Gly	Tyr	Pro	His	Pro	Asp	Trp	Ile	Trp	Arg	Lys	Lys	

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	145	150	155	
	gag aac ggg atg ccc atg gac att gtc aat acc tct ggc cgc ttc ttc			709
	Glu Asn Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe			
	160	165	170	
5	atc atc aac aag gaa aat tac act gag ttg aac att gtg aac ctg cag			757
	Ile Ile Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln			
	175	180	185	190
	atc acg gaa gac cct ggc gag tat gaa tgt aat gcc acc aac gcc att			805
	Ile Thr Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile			
10	195	200	205	
	ggc tcc gcc tct gtt gtc act gtc ctc agg gtg cgg agc cac ctg gcc			853
	Gly Ser Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala			
	210	215	220	
	cca ctc tgg cct ttc ttg gga att ctg gct gaa att atc atc ctt gtg			901
15	Pro Leu Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val			
	225	230	235	
	gtg atc att gtt gtg tat gag aag agg aag agg cca gat gag gtt cct			949
	Val Ile Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro			
	240	245	250	
20	gac gat gat gaa cca gct gga cca atg aaa acc aac tct acc aac aat			997
	Asp Asp Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn			
	255	260	265	270
	cac aaa gat aaa aac ttg cgc cag aga aac aca aat taagtac			1040
	His Lys Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn			
25	275	280		

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	cttggacctc tttggttctc tcccctttca agtgagcaac accacaatga ctgtctaaag	1160
	catgccttat ttagcctctc ctgtaagggt gatctagcca ggtacathtt aaacaatgct	1220
	tcagtgtaga aggtgtaaac tattttgggc ttgatgtgct gtgaatgttg cttttttttt	1280
5	tcctttgtta aaatatttaa atagaagtga aaaggtcctc tgaggatcag atcatgcatg	1340
	cgccattttt tacttaatgc agctgttaaa ttggcaaagc tctaaaatgc actgctgccca	1400
	tctagtata cacttttgta aagtacagca aaacctacag atatatacag tatataaata	1460
	tatatatata tatatttata tttttggggg tgggagaaat ccaaaataaa gtaaatgctt	1520
	gtttcatttt taagctgctg atattcattc cttattgtat gttgtcagat gaggaaattg	1580
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	acctgtgact ttaataagct ggaacagtcc actgaatggg tataatgaat tgcagtatat	1700
	acgtatgatt gctttttaag tgattatctt ttcttctgtt aagtcattga aattcataaa	1760
	tccttttgca ctgatgtgtt gaaccttatt cttgtacatt cattcaatca aggcaaactt	1820
	ttataatttt tcttttgttt ccaatgacct tgaaatgtta tagcatggta atattctatg	1880
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	tgatagattt tataacctaa cggttctcat gcggtgcgta attgtagatg catgtacttg	2000
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	ggatcggcca gagttactcc gaggtg atg agc ctc aac gag cac tcc atg	170
	Met Ser Leu Asn Glu His Ser Met	
	1	5
10	cag gcg ctg tcc tgg cgc aag ctc tac ttg agc cgc gcc aag ctt aaa	218
	Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala Lys Leu Lys	
	10	15
	20	
	gcc tcc agc cgg acc tcg gct ctg ctc tcc ggc ttc gcc atg gtg gca	266
	Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala Met Val Ala	
15	25	30
	35	40
	atg gtg gag gtg cag ctg gac gct gac cac gac tac cca ccg ggg ctg	314
	Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro Pro Gly Leu	
	45	50
	55	
	ctc atc gcc ttc agt gcc tgc acc aca gtg ctg gtg gct gtg cac ctg	362
20	Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala Val His Leu	
	60	65
	70	
	ttt gcg ctc atg atc agc acc tgc atc ctg ccc aac atc gag gcg gtg	410
	Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile Glu Ala Val	
	75	80
	85	
25	agc aac gtg cac aat ctc aac tcg gtc aag gag tcc ccc cat gag cgc	458

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	Ser Asn Val His Asn Leu Asn Ser Val Lys Glu Ser Pro His Glu Arg	
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	atg cac cgc cac atc gag ctg gcc tgg gcc ttc tcc acc gtc atc ggc	506
	Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val Ile Gly	
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	acg ctg ctc ttc cta gct gag gtg gtg ctg ctc tgc tgg gtc aag ttc	554
	Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val Lys Phe	
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	ttg ccc ctc aag aag cag cca ggc cag cca agg ccc acc agc aag ccc	602
10	Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser Lys Pro	
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	ccc gcc agt ggc gca gca gcc aac gtc agc acc agc ggc atc acc ccg	650
	Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile Thr Pro	
	155 160 165	
15	ggc cag gca gct gcc atc gcc tcg acc acc atc atg gtg ccc ttc ggc	698
	Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro Phe Gly	
	170 175 180	
	ctg atc ttt atc gtc ttc gcc gtc cac ttc tac cgc tca ctg gtt agc	746
	Leu Ile Phe Ile Val Phe Ala Val His Phe Tyr Arg Ser Leu Val Ser	
20	185 190 195 200	
	cat aag acc gac cga cag ttc cag gag ctc aac gag ctg gcg gag ttt	794
	His Lys Thr Asp Arg Gln Phe Gln Glu Leu Asn Glu Leu Ala Glu Phe	
	205 210 215	
	gcc cgc tta cag gac cag ctg gac cac aga ggg gac cac ccc ctg acg	842
25	Ala Arg Leu Gln Asp Gln Leu Asp His Arg Gly Asp His Pro Leu Thr	

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	220	225	230	
	ccc ggc agc cac tat gcc taggcccattg tggctctgggc ccttccagtg			890
	Pro Gly Ser His Tyr Ala			
	235			
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	cagggggctg ggcttcagca aggggcagag cgtggaggga agaggatttt tataagagaa			1010
	atttctgcac ttgaaactg tcctctaaga gaataagcat ttctgttct tccagctcca			1070
	ggtccacctc ctgttgggag gcggtggggg gccaaagtgg ggccacacac tcgctgtgtc			1130
	ccctctcctc ccctgtgcca gtgccacctg ggtgcctcct cctgtcctgt ccgtctcaac			1190
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	aggaggtctc tgctgtgat gaagctgtga ccaaacgcac ccaacccttg gcagccatct			120
25	gtccctgcag ccatagccca cattcccatg acctccctct gcttgttttg ggaccatgtc			180

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	tgtacagcct ctaggcccga gccccggagg tgaatgccat gccatgattc tgggtgtgctc	240
	catggcatcc ccagcctagc tcccaatccc actttggcac g atg tta gcc aac	293
	Met Leu Ala Asn	
	1	
5	agc tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct	341
	Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro Asp Tyr Arg Pro	
	5 10 15 20	
	acc cac cgc ctg cac ttg gtg gtc tac agc ttg gtg ctg gct gcc ggg	389
	Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val Leu Ala Ala Gly	
10	25 30 35	
	ctc ccc ctc aac gcg cta gcc ctc tgg gtc ttc ctg cgc gcg ctg cgc	437
	Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu Arg Ala Leu Arg	
	40 45 50	
	gtg cac tcg gtg gtg agc gtg tac atg tgt aac ctg gcg gcc agc gac	485
15	Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu Ala Ala Ser Asp	
	55 60 65	
	ctg ctc ttc acc ctc tcg ctg ccc gtt cgt ctc tcc tac tac gca ctg	533
	Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser Tyr Tyr Ala Leu	
	70 75 80	
20	cac cac tgg ccc ttc ccc gac ctc ctg tgc cag acg acg ggc gcc atc	581
	His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr Thr Gly Ala Ile	
	85 90 95 100	
	ttc cag atg aac atg tac ggc agc tgc atc ttc ctg atg ctc atc aac	629
	Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu Met Leu Ile Asn	
25	105 110 115	

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	gtg gac cgc tac gcc gcc atc gtg cac ccg ctg cga ctg cgc cac ctg	677
	Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg Leu Arg His Leu	
	120 125 130	
	cgg cgg ccc cgc gtg gcg cgg ctg ctc tgc ctg ggc gtg tgg gcg ctc	725
5	Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly Val Trp Ala Leu	
	135 140 145	
	atc ctg gtg ttt gcc gtg ccc gcc gcc cgc gtg cac agg ccc tcg cgt	773
	Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His Arg Pro Ser Arg	
	150 155 160	
10	tgc cgc tac cgg gac ctc gag gtg cgc cta tgc ttc gag agc ttc agc	821
	Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe Glu Ser Phe Ser	
	165 170 175 180	
	gac gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag	869
	Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu	
15	185 190 195	
	gcg ctg ggc ttc ctg ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc	917
	Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly	
	200 205 210	
	cga gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg	965
20	Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg	
	215 220 225	
	cgg cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg	1013
	Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu	
	230 235 240	
25	ctg tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg	1061

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 Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg
 5 265 270 275
 ggg gtg ctg atg gtg atg gtg ctg ctg gcc ggc gcc aac tgc gtg ctg 1157
 Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu
 280 285 290
 gac ccg ctg gtg tac tac ttt agc gcc gag ggc ttc cgc aac acc ctg 1205
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 295 300 305
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 Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly
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 15 acg cgg gcg gcg ctc gcg caa tcc gaa agg tcc gcc gtc acc acc gac 1301
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 325 330 335 340
 gcc acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac 1349
 Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp
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 tcc cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc 1397
 Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu
 360 365 370
 tga acacacatgc cattgcgctg tccgtgcccg actcccaacg cctctcgttc 1450
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<213> Homo sapiens

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<222> (25)... (465)

15

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5

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20

Gly Ala Ala Ala Leu Gly Gly Ala Leu Phe Leu Leu Leu Phe Ala Leu

10

15

20

25

ggg gtc cgc cag ctg ctg aag cag agg cgg ccg atg ggc ttc ccc ccg 147

Gly Val Arg Gln Leu Leu Lys Gln Arg Arg Pro Met Gly Phe Pro Pro

30

35

40

25

ggg ccg ccg ggg ctg cca ttt atc ggc aac atc tat tcc ctg gca gcc 195

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Gly Pro Pro Gly Leu Pro Phe Ile Gly Asn Ile Tyr Ser Leu Ala Ala
 45 50 55
 tca tcc gag ctt ccc cat gtc tac atg aga aag cag agc cag gtg tac 243
 Ser Ser Glu Leu Pro His Val Tyr Met Arg Lys Gln Ser Gln Val Tyr
 5 60 65 70
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 Gly Glu Val Gln Pro Arg Arg Ala Pro Gly Arg Glu Gly Arg Gln Ala
 75 80 85
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 10 Gly Pro Gly Trp Pro Gly Pro Ser Trp Leu Asp Leu Trp Pro Pro Leu
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 Gly Arg Leu Val Gly Thr Ser Pro Cys Ala Gly Cys Pro Leu Arg Asp
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 15 acc cgc ttc ccg ggt ctg gaa ggg aga agt cct cga cgc cgt gcc ccc 435
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 Leu Gln Gly Glu Pro Arg Pro Cys Arg
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<220>

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<222> (268)... (1176)

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aatctggaag ggcggtgaaa aacctacgtc ctgccctcgc ccggcctctc cattcgtccc 180

15 ccgggtagag aggtgcccgg ctcccacccc ttcccagccc cagccctgga gacagcagcc 240

cctagactac tgagggacag cgacagc atg aag gct ccg ggt cgg ctc gtg 291

Met Lys Ala Pro Gly Arg Leu Val

1

5

ctc atc atc ctg tgc tcc gtg gtc ttc tct gcc gtc tac atc ctc ctg 339

20 Leu Ile Ile Leu Cys Ser Val Val Phe Ser Ala Val Tyr Ile Leu Leu

10

15

20

tgc tgc tgg gcc ggc ctg ccc ctc tgc ctg gcc acc tgc ctg gac cac 387

Cys Cys Trp Ala Gly Leu Pro Leu Cys Leu Ala Thr Cys Leu Asp His

25

30

35

40

25 cac ttc ccc aca ggc tcc agg ccc act gtg ccg gga ccc ctg cac ttc 435

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His Phe Pro Thr Gly Ser Arg Pro Thr Val Pro Gly Pro Leu His Phe
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 agt gga tat agc agt gtg cca gat ggg aag ccg ctg gtc cgc gag ccc 483
 Ser Gly Tyr Ser Ser Val Pro Asp Gly Lys Pro Leu Val Arg Glu Pro
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 Cys Arg Ser Cys Ala Val Val Ser Ser Ser Gly Gln Met Leu Gly Ser
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 90 95 100
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	185	190	195	200
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	Gly Lys Asn Arg Arg Gln Ser Gly Ser Phe Leu Ser Thr Gly Trp Phe			
	205	210	215	
	acc atg atc ctc gcg ctg gag ctg tgt gag gag atc gtg gtc tat ggg			963
	Thr Met Ile Leu Ala Leu Glu Leu Cys Glu Glu Ile Val Val Tyr Gly			
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	atg gtc agc gac agc tac tgc agg gag aag agc cac ccc tca gtg cct			1011
	Met Val Ser Asp Ser Tyr Cys Arg Glu Lys Ser His Pro Ser Val Pro			
	235	240	245	
	tac cac tac ttt gag aag ggc cgg cta gat gag tgt cag atg tac ctg			1059
15	Tyr His Tyr Phe Glu Lys Gly Arg Leu Asp Glu Cys Gln Met Tyr Leu			
	250	255	260	
	gca cac gag cag gcg ccc cga agc gcc cac cgc ttc atc act gag aag			1107
	Ala His Glu Gln Ala Pro Arg Ser Ala His Arg Phe Ile Thr Glu Lys			
	265	270	275	280
20	gcg gtc ttc tcc cgc tgg gcc aag aag agg ccc atc gtg ttc gcc cat			1155
	Ala Val Phe Ser Arg Trp Ala Lys Lys Arg Pro Ile Val Phe Ala His			
	285	290	295	
	ccg tcc tgg agg act gag tagcttcogt cgtcctgccca gccgccatgc cgttgcg			1210
	Pro Ser Trp Arg Thr Glu			
25	300			

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 <212> DNA
 <213> Homo sapiens

15 <220>
 <221> CDS
 <222> (246)... (830)

<400> 28

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 aggactctat ataaatcgct gtgggctcac cacctctaag gaggagcact gactgaagac 120
 agaaaaattg atgaactgaa gaagacatgg tccattatgc cttacaaact tacacagtgc 180
 tttgggaatt ccaaagtact cagtggagag aggtgtttca ggagccgtag agccagatcg 240
 tcatc atg tct gca ttg tgg ctg ctg ctg ggc ctc ctt gcc ctg atg 287

25 Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met

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	1	5	10	
	gac ttg tct gaa agc agc aac tgg gga tgc tat gga aac atc caa agc 335			
	Asp Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser			
	15	20	25	30
5	ctg gac acc cct gga gca tct tgt ggg att gga aga cgt cac ggc ctg 383			
	Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu			
	35	40	45	
	aac tac tgt gga gtt cgt gct tct gaa agg ctg gct gaa ata gac atg 431			
	Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met			
10	50	55	60	
	cca tac ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag 479			
	Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys			
	65	70	75	
	tac tgc atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct 527			
15	Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser			
	80	85	90	
	ccc ggt gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg 575			
	Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val			
	95	100	105	110
20	cag gac cct ggc tct caa gct ccc aca tcc tgg att agt gag tct cag 623			
	Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln			
	115	120	125	
	gtt tcc cag aca act gaa gtt ctg act act aga atc aaa gaa atc cag 671			
	Val Ser Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln			
25	130	135	140	

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agg agg ttt cca acc tgg acc cct gac cag tac ctg aga ggt gga ctc 719
 Arg Arg Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu
 145 150 155

tgt gcc tac agt ggg ggt gct ggc tat gtc cga agc agc cag gac ctg 767
 5 Cys Ala Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu
 160 165 170

agc tgt gac ttc tgc aat gat gtc ctt gca cga gcc aag tac ctc aag 815
 Ser Cys Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys
 175 180 185 190

10 aga cat ggc ttc taacatctca gatgaaaccc aagaccatga tcacatatgc agc 870
 Arg His Gly Phe

ctcaaattgtt acacagataa aactagccaa gggcacctgt aactgggaat ctgagtttga 930
 cctaaaagtc attaaaataa catgaatcac att 963

15

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 <211> 2667
 <212> DNA
 <213> Homo sapiens

20

<220>
 <221> CDS
 <222> (229)... (1857)

25 <400> 29

52 / 59

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	tttcaaaaat ggagaagaca gatcacagcc actgaccagg gaccgtggga ggtgccacgt	120
	gatggtgagg catcatgcta gggagctgag ctctgacctt cctgctgggt gattctccac	180
	ctctgggctg ctagatctac ttcttgatg ccgtgaagat cctcatgt atg aaa	234
5	Met Lys	
	1	
	atg aag tcc cag gca acc atg att tgc tgc tta gtg ttc ttt ctg tcc	282
	Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe Leu Ser	
	5 10 15	
10	aca gaa tgt tcc cac tat aga tcc aag att cac cta aaa agc tat agt	330
	Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser Tyr Ser	
	20 25 30	
	gaa gtg gcc aac cac atc ctc gac aca gca gcc att tca aac tgg gct	378
	Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala	
15	35 40 45 50	
	ttc att ccc aac aaa aat gcc agc tcg gat ttg ttg cag tca gtg aat	426
	Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn	
	55 60 65	
	ttg ttt gcc aga caa ctc cac atc cac aat aat tct gag aac att gtg	474
20	Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val	
	70 75 80	
	aat gaa ctc ttc att cag aca aaa ggg ttt cac atc aac cat aat acc	522
	Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr	
	85 90 95	
25	tca gag aaa agc ctc aat ttc tcc atg agc atg aac aat acc aca gaa	570

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	Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu	
	100 105 110	
	gat atc tta gga atg gta cag att ccc agg caa gag cta agg aag ctg	618
	Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu	
5	115 120 125 130	
	tgg cca aat gca tcc caa gcc att agc ata gct ttc cca acc ttg ggg	666
	Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly	
	135 140 145	
	gct atc ctg aga gaa gcc cac ttg caa aat gtg agt ctt ccc aga cag	714
10	Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln	
	150 155 160	
	gta aat ggt ctg gtg cta tca gtg gtt tta cca gaa agg ttg caa gaa	762
	Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu	
	165 170 175	
15	atc ata ctc acc ttc gaa aag atc aat aaa acc cgc aat gcc aga gcc	810
	Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala	
	180 185 190	
	cag tgt gtt ggc tgg cac tcc aag aaa agg aga tgg gat gag aaa gcg	858
	Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala	
20	195 200 205 210	
	tgc caa atg atg ttg gat atc agg aac gaa gtg aaa tgc cgc tgt aac	906
	Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn	
	215 220 225	
	tac acc agt gtg gtg atg tct ttt tcc att ctc atg tcc tcc aaa tcg	954
25	Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser	

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	230	235	240	
	atg acc gac aaa gtt ctg gac tac atc acc tgc att ggg ctc agc gtc			1002
	Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val			
	245	250	255	
5	tca atc cta agc ttg gtt ctt tgc ctg atc att gaa gcc aca gtg tgg			1050
	Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp			
	260	265	270	
	tcc cgg gtg gtt gtg acg gag ata tca tac atg cgt cac gtg tgc atc			1098
	Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val Cys Ile			
10	275	280	285	290
	gtg aat ata gca gtg tcc ctt ctg act gcc aat gtg tgg ttt atc ata			1146
	Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe Ile Ile			
	295	300	305	
	ggc tct cac ttt aac att aag gcc cag gac tac aac atg tgt gtt gca			1194
15	Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys Val Ala			
	310	315	320	
	gtg aca ttt ttc agc cac ttt ttc tac ctc tct ctg ttt ttc tgg atg			1242
	Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe Trp Met			
	325	330	335	
20	ctc ttc aaa gca ttg ctc atc att tat gga ata ttg gtc att ttc cgt			1290
	Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile Phe Arg			
	340	345	350	
	agg atg atg aag tcc cga atg atg gtc att ggc ttt gcc att ggc tat			1338
	Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile Gly Tyr			
25	355	360	365	370

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	ggg tgc cca ttg atc att gct gtc act aca gtt gct atc aca gag cca	1386
	Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro	
	375 380 385	
	gag aac ggc tac atg aga cct gag gcc tgt tgg ctt aac tgg gac aat	1434
5	Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn	
	390 395 400	
	acc aaa gcc ctt tta gca ttt gcc atc ccg gcg ttc gtc att gtg gct	1482
	Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala	
	405 410 415	
10	gta aat ctg att gtg gtt ttg gtt gtt gct gtc aac act cag agg ccc	1530
	Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln Arg Pro	
	420 425 430	
	tct att ggc agt tcc aag tct cag gat gtg gtc ata att atg agg atc	1578
	Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile	
15	435 440 445 450	
	agc aaa aat gtt gcc atc ctc act cca ctg ctg gga ctg acc tgg ggt	1626
	Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly	
	455 460 465	
	ttt gga ata gcc act ctc ata gaa ggc act tcc ttg acg ttc cat ata	1674
20	Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile	
	470 475 480	
	att ttt gcc ttg ctc aat gct ttc cag ggt ttt ttc atc ctg ctg ttt	1722
	Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu Leu Phe	
	485 490 495	
25	gga acc att atg gat cac aag ata aga gat gct ttg agg atg agg atg	1770

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Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met Arg Met

500

505

510

tct tca ctg aag ggg aaa tcg agg gca gct gag aat gca tca cta ggc 1818

Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser Leu Gly

5

515

520

525

530

cca acc aat gga tct aaa tta atg aat cgt caa gga tgaaatgctg ccccat 1870

Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly

535

540

ttctcatgga tgtcctgaga ccaagagggg agatccagga gaaagaggcc atggaaagca 1930

10

ggctggagtg aggaggaatg gtcatgcttc cttggaagac tttctcttct tgtcaggagt 1990

gactcccaag ctcttggtcg gccgaagaaa aactgaggat aacatttgct gactgggctt 2050

taaggagcat gatttatgga ccccttaacc taccctgccc ctgcaagagg ctggcttctt 2110

ggatcaatctt gactagatta agagtcaatc tgcaagccat tttatggctt ccctggccag 2170

ctgggggctg tagggccctg ctgggcttgg tcgtctttca ctctgaggc ctgctctgtg 2230

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gtccatagc tcagtcctcc atcactctgc gtggatcctg ggtactttgg acagtgaggg 2290

ttcgatccaa ttttaggggt aggggtgggg gtgggagtg gagtggtgggt tggcaggagg 2350

aagaatgagt ctactttgga gacaattaag tcatggtacg tttcctaaag atagggaacg 2410

gaagaaaagc aagagaactg ttaatatgc tgattatatt agtctatatt agaccttgag 2470

taactaatt tagcttctag gatccaagtt tccttatttg tgaaacagga aaaaaaatt 2530

20

ctttaggta ttactgtttg tgtgtttgag ttactgcac atgtttgtgt ttgtgtatat 2590

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<210> 30

25

<211> 1478

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<212> DNA

<213> Homo sapiens

<220>

5 <221> CDS

<222> (174)... (1004)

<400> 30

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	cagcccgaag cagccagacc agcccctgag cctcccgggt gctggcagct gtc atg	176
	Met	
	1	
	ggg cta ccc tgg ggg cag cct cac cta ggg ctg cag atg ctc ctc ctg	224
15	Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu Leu	
	5 10 15	
	gcg ttg aac tgt ctc cgg ccc agc ctg agc ctg gag ctg gtg ccc tac	272
	Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro Tyr	
	20 25 30	
20	aca cca cag ata aca gct tgg gac ctg gaa ggg aag gtc aca gcc acc	320
	Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala Thr	
	35 40 45	
	acc ttc tcc ctg gag cag ccg cgc tgt gtc ttc gat ggg ctt gcc agc	368
	Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala Ser	
25	50 55 60 65	

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	gcc agc gat acc gtc tgg ctc gtg gtg gcc ttc agc aat gcc tcc agg	416
	Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser Arg	
	70 75 80	
	ggc ttc cag aac ccg gag aca ctg gct gac att ccg gcc tcc cca cag	464
5	Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro Gln	
	85 90 95	
	ctg ctg acc gat ggc cac tac atg acg ctg ccc ctg tct ccg gac cag	512
	Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp Gln	
	100 105 110	
10	ctg ccc tgt ggc gac ccc atg gcg ggc agc gga ggc gcc ccc gtg ctg	560
	Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val Leu	
	115 120 125	
	cgg gtg ggc cat gac cac ggc tgc cac cag cag ccc ttc tgc aac gcg	608
	Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn Ala	
15	130 135 140 145	
	ccc ctc cct ggc cct gga ccc tat cgg gtg aag ttc ctc ctg atg gac	656
	Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met Asp	
	150 155 160	
	acc agg ggc tca ccc agg gct gag acc aag tgg tca gac ccc atc act	704
20	Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile Thr	
	165 170 175	
	ctc cac caa ggg aag acc ccc gga tcc atc gac acc tgg cca ggg cgg	752
	Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly Arg	
	180 185 190	
25	cga agt ggc agc atg atc gtc att acc tcc atc ctc tct tct ctg gcc	800

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Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu Ala
 195 200 205
 ggc ctc cta ctc ttg gcc ttc ttg gca gcc tct acc atg cgc ttc tcc 848
 Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe Ser
 5 210 215 220 225
 agc ctg tgg tgg ccg gag gag gcc ccg gag cag ctg cgg atc ggc tcc 896
 Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly Ser
 230 235 240
 ttc atg ggc aag cgc tac atg acc cac cac atc cca ccc agc gag gcc 944
 10 Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu Ala
 245 250 255
 gcc aca ctg ccg gtg ggc tgc aag cct ggc ctg gac ccc ctc ccc agc 992
 Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro Ser
 260 265 270
 15 ctc agc ccc tagcctggcc tctttgcatg gggtctggggg agatggggc 1040
 Leu Ser Pro
 275
 gccgggagtg agtgcattgt gctttgtccc agctcctgca cccacaggcc cctcagggc 1100
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